CRF Errors Corrected by the STIC Systems Branch

ENTERED

Serial Number: _09/155, 252A_

CRF Processing Date: _2/12/2001_
Edited by: _____
Verified by: _____

STIC staff

TECHNOLOGY CENTER 1600/2900

JUL 16 2001

RECEIVED

☐ Changed a file from non-ASCII to ASCII

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

'Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

#16

RAW SEQUENCE LISTING   DATE: 07/12/2001
·PATENT APPLICATION: US/09/155,252A   TIME: 17:47:04

Input Set : **A:\Pto.amc**
Output Set: **N:\CRF3\07122001\I155252A.raw**

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 3 <110> APPLICANT: EVANS, Ronald
 4        FORMAN, Barry
 6 <120> TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED
 7        RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF
 9 <130> FILE REFERENCE: SALK1470-2
11 <140> CURRENT APPLICATION NUMBER: US 09/155,252A
12 <141> CURRENT FILING DATE: 1998-09-21
14 <150> PRIOR APPLICATION NUMBER: PCT/US96/05465
15 <151> PRIOR FILING DATE: 1996-04-18
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2005
23 <212> TYPE: DNA
24 <213> ORGANISM: Mus Musculus
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (352)..(1776)
30 <400> SEQUENCE: 1
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34 ggaggacgcg gaagaagaga cctggggcgc tgcctggggt attgggtcgc gcgcagtgag     120
36 gggaccgagt gtgacgacaa ggtgaccggg ctgaggggac gggctgagga gaagtcacac     180
38 tctgacagga gcctgtgaga ccaacagcct gacggggtct cggttgaggg gacgcgggct     240
40 gagaagtcac gttctgacag gactgtgtga cagacaagat ttgaaagaag cggtgaacca     300
42 ctgatattca ggacattttt aaaaacaaga ctacccttta ctgaaattac c atg gtt     357
43                                                           Met Val
44                                                           1
46 gac aca gag atg cca ttc tgg ccc acc aac ttc gga atc agc tct gtg     405
47 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
48         5                   10                  15
50 gac ctc tcc gtg atg gaa gac cac tcg cat tcc ttt gac atc aag ccc     453
51 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
52     20                  25                  30
54 ttt acc aca gtt gat ttc tcc agc att tct gct cca cac tat gaa gac     501
55 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Ala Pro His Tyr Glu Asp
56 35                  40                  45                  50
58 att cca ttc aca aga gct gac cca atg gtt gct gat tac aaa tat gac     549
59 Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys Tyr Asp
60                 55                  60                  65
62 ctg aag ctc caa gaa tac caa agt gcg atc aaa gta gaa cct gca tct     597
63 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
64             70                  75                  80
66 cca cct tat tat tct gaa aag acc cag ctc tac aac agg cct cat gaa     645
67 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Pro His Glu
68             85                  90                  95
70 gaa cct tct aac tcc ctc atg gcc att gag tgc cga gtc tgt ggg gat     693
71 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
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RAW SEQUENCE LISTING   DATE: 07/12/2001
PATENT APPLICATION: US/09/155,252A   TIME: 17:47:04

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07122001\I155252A.raw

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74 aaa gca tca ggc ttc cac tat gga gtt cat gct tgt gaa gga tgc aag      741
75 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
76 115                    120                    125                    130
78 ggt ttt ttc cga aga acc atc cga ttg aag ctt att tat gat agg tgt      789
79 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
80                    135                    140                    145
82 gat ctt aac tgc cgg atc cac aaa aaa agt aga aat aaa tgt cag tac      837
83 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
84            150                    155                    160
86 tgt cgg ttt cag aag tgc ctt gct gtg ggg atg tct cac aat gcc atc      885
87 Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
88            165                    170                    175
90 agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag      933
91 Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
92      180                    185                    190
94 atc tcc agt gat atc gac cag ctg aac cca gag tct gct gat ctg cga      981
95 Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
96 195                    200                    205                    210
98 gcc ctg gca aag cat ttg tat gac tca tac ata aag tcc ttc ccg ctg     1029
99 Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu
100                   215                    220                    225
102 acc aaa gcc aag gcg agg gcg atc ttg aca gga aag aca acg gac aaa     1077
103 Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys
104            230                    235                    240
106 tca cca ttt gtc atc tac gac atg aat tcc tta atg atg gga gaa gat     1125
107 Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp
108            245                    250                    255
110 aaa atc aag ttc aaa cat atc acc ccc ctg cag gag cag agc aaa gag     1173
111 Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu
112      260                    265                    270
114 gtg gcc atc cga att ttt caa ggg tgc cag ttt cga tcc gta gaa gcc     1221
115 Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala
116 275                    280                    285                    290
118 gtg caa gag atc aca gag tat gcc aaa aat atc cct ggt ttc att aac     1269
119 Val Gln Glu Ile Thr Glu Tyr Ala Lys Asn Ile Pro Gly Phe Ile Asn
120                   295                    300                    305
122 ctt gat ttg aat gac caa gtg act ctg ctc aag tat ggt gtc cat gag     1317
123 Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
124            310                    315                    320
126 atc atc tac acg atg ctg gcc tcc ctg atg aat aaa gat gga gtc ctc     1365
127 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
128      325                    330                    335
130 atc tca gag ggc caa gga ttc atg acc agg gag ttc ctc aaa agc ctg     1413
131 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
132      340                    345                    350
134 cgg aag ccc ttt ggt gac ttt atg gag cct aag ttt gag ttt gct gtg     1461
135 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
136 355                    360                    365                    370
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Input Set : **A:\Pto.amc**
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138 aag ttc aat gca ctg gaa tta gat gac agt gac ttg gct ata ttt ata      1509
139 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
140              375                380                385
142 gct gtc att att ctc agt gga gac cgc cca ggc ttg ctg aac gtg aag      1557
143 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
144              390                395                400
146 ccc atc gag gac atc caa gac aac ctg ctg cag gcc ctg gaa ctg cag      1605
147 Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
148              405                410                415
150 ctc aag ctg aat cac cca gag tcc tct cag ctg ttc gcc aag gtg ctc      1653
151 Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Val Leu
152      420                425                430
154 cag aag atg aca gac ctc agg cag atc gtc aca gag cac gtg cag cta      1701
155 Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
156 435                440                445                450
158 ctg cat gtg atc aag aag aca gag aca gac atg agc ctt cac ccc ctg      1749
159 Leu His Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
160              455                460                465
162 ctc cag gag atc tac aag gac ttg tat tagcaggaaa gtcccacccg           1796
163 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
164              470                475
166 ctgacaacgt gttccttcta ttgattgcac tattattttg agggaaaaaa atctgacacc   1856
168 taagaaattt actgtgaaaa agcatttaaa aacaaaaagt tttagaacat gatctatttt   1916
170 atgcatattg tttataaaga tacatttaca atttactttt aatattaaaa attaccacat   1976
172 tataaaaaaa aaaaaaaaaa aggaattcc                                     2005
176 <210> SEQ ID NO: 2
177 <211> LENGTH: 475
178 <212> TYPE: PRT
179 <213> ORGANISM: Mus Musculus
181 <400> SEQUENCE: 2
184 Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser
185 1              5                10                15
188 Ser Val Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile
189              20                25                30
192 Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Ala Pro His Tyr
193              35                40                45
196 Glu Asp Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys
197      50                55                60
200 Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro
201 65                70                75                80
204 Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Pro
205              85                90                95
208 His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys
209              100                105                110
212 Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly
213              115                120                125
216 Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp
217      130                135                140
220 Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys
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221 145                    150                   155                   160
224 Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
225                 165                   170                   175
228 Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu
229                 180                   185                   190
232 Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp
233         195                   200                   205
236 Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe
237      210                   215                   220
240 Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr
241 225                   230                   235                   240
244 Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly
245                 245                   250                   255
248 Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser
249                 260                   265                   270
252 Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val    .
253         275                   280                   285
256 Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Asn Ile Pro Gly Phe
257      290                   295                   300
260 Ile Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val
261 305                   310                   315                   320
264 His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly
265                 325                   330                   335
268 Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys
269                 340                   345                   350
272 Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe
273         355                   360                   365
276 Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile
277      370                   375                   380
280 Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn
281 385                   390                   395                   400
284 Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
285                 405                   410                   415
288 Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys
289         420                   425                   430
292 Val Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val
293         435                   440                   445          .
296 Gln Leu Leu His Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His
297      450                   455                   460
300 Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
301 465                   470                   475
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304 <210> SEQ ID NO: 3
305 <211> LENGTH: 546
306 <212> TYPE: DNA
307 <213> ORGANISM: Saccharomyces cerevisiae
309 <220> FEATURE:
310 <221> NAME/KEY: CDS
311 <222> LOCATION: (35)..(544)
313 <400> SEQUENCE: 3

RAW SEQUENCE LISTING   DATE: 07/12/2001
PATENT APPLICATION: US/09/155,252A   TIME: 17:47:04

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07122001\I155252A.raw

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315 gggagaccca agcttgaagc aagcctcctg aaag atg aag cta ctg tct tct atc       55
316                                        Met Lys Leu Leu Ser Ser Ile
317                                        1               5
319 gaa caa gca tgc gat att tgc cga ctt aaa aag ctc aag tgc tcc aaa         103
320 Glu Gln Ala Cys Asp Ile Cys Arg Leu Lys Lys Leu Lys Cys Ser Lys
321          10              15                  20
323 gaa aaa ccg aag tgc gcc aag tgt ctg aag aac aac tgg gag tgt cgc         151
324 Glu Lys Pro Lys Cys Ala Lys Cys Leu Lys Asn Asn Trp Glu Cys Arg
325          25              30                  35
327 tac tct ccc aaa acc aaa agg tct ccg ctg act agg gca cat ctg aca         199
328 Tyr Ser Pro Lys Thr Lys Arg Ser Pro Leu Thr Arg Ala His Leu Thr
329 40              45                  50                  55
331 gaa gtg gaa tca agg cta gaa aga ctg gaa cag cta ttt cta ctg att         247
332 Glu Val Glu Ser Arg Leu Glu Arg Leu Glu Gln Leu Phe Leu Leu Ile
333              60                  65                  70
335 ttt cct cga gaa gac ctt gac atg att ttg aaa atg gat tct tta cag         295
336 Phe Pro Arg Glu Asp Leu Asp Met Ile Leu Lys Met Asp Ser Leu Gln
337              75                  80                  85
339 gat ata aaa gca ttg tta aca gga tta ttt gta caa gat aat gtg aat         343
340 Asp Ile Lys Ala Leu Leu Thr Gly Leu Phe Val Gln Asp Asn Val Asn
341          90                  95                  100
343 aaa gat gcc gtc aca gat aga ttg gct tca gtg gag act gat atg cct         391
344 Lys Asp Ala Val Thr Asp Arg Leu Ala Ser Val Glu Thr Asp Met Pro
345          105                 110                 115
347 cta aca ttg aga cag cat aga ata agt gcg aca tca tca tcg gaa gag         439
348 Leu Thr Leu Arg Gln His Arg Ile Ser Ala Thr Ser Ser Ser Glu Glu
349 120                 125                 130                 135
351 agt agt aac aaa ggt caa aga cag ttg act gta tcg ccg gaa ttc ccg         487
352 Ser Ser Asn Lys Gly Gln Arg Gln Leu Thr Val Ser Pro Glu Phe Pro
353                  140                 145                 150
355 ggg atc cgt cga cgg tac cag ata tca gga tcc tgg cca gct agc tag         535
356 Gly Ile Arg Arg Arg Tyr Gln Ile Ser Gly Ser Trp Pro Ala Ser
357              155                 160                 165
359 gta gct aga gg                                                          546
360 Val Ala Arg
364 <210> SEQ ID NO: 4
365 <211> LENGTH: 166
366 <212> TYPE: PRT
367 <213> ORGANISM: Saccharomyces cerevisiae
369 <400> SEQUENCE: 4
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373 1               5                   10                  15
376 Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
377              20                  25                  30
380 Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
381          35                  40                  45
384 Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
385      50                  55                  60
388 Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/155,252A

DATE: 07/12/2001
TIME: 17:47:05

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07122001\I155252A.raw